

SEQUENCE LISTING

<110> BASF AG

<120> Method for producing carotenoids or their precursors
using genetically modified organisms of the Blakeslea genus,
carotenoids or their precursors produced by said method and
use thereof

<130> BASF/NAE877/03

<160> 80

<170> PatentIn version 3.2

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<212> DNA

<213> Artificial

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<220>
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<220>
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<220>
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<211> 1771

<212> DNA

<213> Haematococcus pluvialis

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<222> (166)..(1155)

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120

ccgcgagtct cccgccgcac tgactgccat agcacagcta gacga atg cag cta gca

177

Met Gln Leu Ala

1

gcg aca gta atg ttg gag cag ctt acc gga agc gct gag gca ctc aag

225

Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala Glu Ala Leu Lys

5

10

15

20

gag aag gag aag gag gtt gca ggc agc tct gac gtg ttg cgt aca tgg

273

Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val Leu Arg Thr Trp

25

30

35

gcg acc cag tac tcg ctt ccg tca gaa gag tca gac gcg gcc cgc ccg

321

Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp Ala Ala Arg Pro

40

45

50

gga ctg aag aat gcc tac aag cca cca cct tcc gac aca aag ggc atc	369
Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp Thr Lys Gly Ile	
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aca atg gcg cta cgt gtc atc ggc tcc tgg gcc gca gtg ttc ctc cac	417
Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala Val Phe Leu His	
70 75 80	
gcc att ttt caa atc aag ctt ccg acc tcc ttg gac cag ctg cac tgg	465
Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp Gln Leu His Trp	
85 90 95 100	
ctg ccc gtg tca gat gcc aca gct cag ctg gtt agc ggc acg agc agc	513
Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser Gly Thr Ser Ser	
105 110 115	
ctg ctc gac atc gtc gta gta ttc ttt gtc ctg gag ttc ctg tac aca	561
Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu Phe Leu Tyr Thr	
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ggc ctt ttt atc acc acg cat gat gct atg cat ggc acc atc gcc atg	609
Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly Thr Ile Ala Met	
135 140 145	
aga aac agg cag ctt aat gac ttc ttg ggc aga gta tgc atc tcc ttg	657
Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val Cys Ile Ser Leu	
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tac gcc tgg ttt gat tac aac atg ctg cac cgc aag cat tgg gag cac	705
Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys His Trp Glu His	
165 170 175 180	
cac aac cac act ggc gag gtg ggc aag gac cct gac ttc cac agg gga	753
His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Arg Gly	
185 190 195	
aac cct ggc att gtg ccc tgg ttt gcc agc ttc atg tcc agc tac atg	801
Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met	
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tcg atg tgg cag ttt gcg cgc ctc gca tgg tgg acg gtg gtc atg cag	849
Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr Val Val Met Gln	
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ctg ctg ggt gcg cca atg gcg aac ctg ctg gtg ttc atg gcg gcc gcg	897
Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala	
230 235 240	
ccc atc ctg tcc gcc ttc cgc ttg ttc tac ttt ggc acg tac atg ccc	945
Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Met Pro	
245 250 255 260	
cac aag cct gag cct ggc gcc gcg tca ggc tct tca cca gcc gtc atg	993
His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser Pro Ala Val Met	
265 270 275	
aac tgg tgg aag tcg cgc act agc cag gcg tcc gac ctg gtc agc ttt	1041
Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp Leu Val Ser Phe	
280 285 290	
ctg acc tgc tac cac ttc gac ctg cac tgg gag cac cac cgc tgg ccc	1089
Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His His Arg Trp Pro	
295 300 305	
ttc gcc ccc tgg tgg gag ctg ccc aac tgc cgc cgc ctg tct ggc cga	1137
Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg Leu Ser Gly Arg	
310 315 320	
ggt ctg gtt cct gcc tag ctggacacac tgcagtgggc cctgctgcca	1185
Gly Leu Val Pro Ala	
325	
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<211> 329
<212> PRT
<213> Haematococcus pluvialis

<400> 12

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Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp
35 40 45

Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
50 55 60

Thr Lys Gly Ile Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala
65 70 75 80

Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
85 90 95

Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
100 105 110

Gly Thr Ser Ser Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu
115 120 125

Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
130 135 140

Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
145 150 155 160

Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
165 170 175

His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
180 185 190

Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
195 200 205

Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
210 215 220

Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
225 230 235 240

Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
245 250 255

Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
260 265 270

Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
275 280 285

Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
290 295 300

His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg
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Leu Ser Gly Arg Gly Leu Val Pro Ala
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<212> DNA
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<220>
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Met His Val

gca tcg gca cta atg gtc gag cag aaa ggc agt gag gca gct gct tcc	224
Ala Ser Ala Leu Met Val Glu Gln Lys Gly Ser Glu Ala Ala Ala Ser	
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agc cca gac gtc ttg aga gcg tgg gcg aca cag tat cac atg cca tcc	272
Ser Pro Asp Val Leu Arg Ala Trp Ala Thr Gln Tyr His Met Pro Ser	
20 25 30 35	
gag tcg tca gac gca gct cgt cct gcg cta aag cac gcc tac aaa cct	320
Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala Tyr Lys Pro	
40 45 50	
cca gca tct gac gcc aag ggc atc acg atg gcg ctg acc atc att ggc	368
Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr Ile Ile Gly	
55 60 65	
acc tgg acc gca gtg ttt tta cac gca ata ttt caa atc agg cta ccg	416
Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile Arg Leu Pro	
70 75 80	
aca tcc atg gac cag ctt cac tgg ttg cct gtg tcc gaa gcc aca gcc	464
Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu Ala Thr Ala	
85 90 95	
cag ctt ttg ggc gga agc agc agc cta ctg cac atc gct gca gtc ttc	512
Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala Ala Val Phe	
100 105 110 115	
att gta ctt gag ttc ctg tac act ggt cta ttc atc acc aca cat gac	560
Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp	
120 125 130	
gca atg cat ggc acc ata gct ttg agg cac agg cag ctc aat gat ctc	608
Ala Met His Gly Thr Ile Ala Leu Arg His Arg Gln Leu Asn Asp Leu	
135 140 145	
ctt ggc aac atc tgc ata tca ctg tac gcc tgg ttt gac tac agc atg	656
Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Ser Met	
150 155 160	
ctg cat cgc aag cac tgg gag cac cac aac cat act ggc gaa gtg ggg	704

Leu His Arg Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly	
165	170 175
aaa gac cct gac ttc cac aag gga aat ccc ggc ctt gtc ccc tgg ttc	752
Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe	
180	185 190 195
gcc agc ttc atg tcc agc tac atg tcc ctg tgg cag ttt gcc cgg ctg	800
Ala Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu	
	200 205 210
gca tgg tgg gca gtg gtg atg caa atg ctg ggg gcg ccc atg gca aat	848
Ala Trp Trp Ala Val Val Met Gln Met Leu Gly Ala Pro Met Ala Asn	
	215 220 225
ctc cta gtc ttc atg gct gca gcc cca atc ttg tca gca ttc cgc ctc	896
Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu	
	230 235 240
ttc tac ttc ggc act tac ctg cca cac aag cct gag cca ggc cct gca	944
Phe Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala	
	245 250 255
gca ggc tct cag gtg atg gcc tgg ttc agg gcc aag aca agt gag gca	992
Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr Ser Glu Ala	
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tct gat gtg atg agt ttc ctg aca tgc tac cac ttt gac ctg cac tgg	1040
Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp	
	280 285 290
gag cac cac agg tgg ccc ttt gcc ccc tgg tgg cag ctg ccc cac tgc	1088
Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu Pro His Cys	
	295 300 305
cgc cgc ctg tcc ggg cgt ggc ctg gtg cct gcc ttg gca tga	1130
Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Leu Ala	
	310 315 320
cctggtcctt ccgctggtga cccagcgtct gcacaagagt gtcattgctac aggggtgctgc	1190

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<210> 14
<211> 320
<212> PRT
<213> Haematococcus pluvialis

<400> 14

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Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala
35 40 45

Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr
50 55 60

Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile

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Ala	Thr	Ala	Gln	Leu	Leu	Gly	Gly	Ser	Ser	Ser	Leu	Leu	His	Ile	Ala
				100					105					110	
Ala	Val	Phe	Ile	Val	Leu	Glu	Phe	Leu	Tyr	Thr	Gly	Leu	Phe	Ile	Thr
				115					120					125	
Thr	His	Asp	Ala	Met	His	Gly	Thr	Ile	Ala	Leu	Arg	His	Arg	Gln	Leu
				130					135					140	
Asn	Asp	Leu	Leu	Gly	Asn	Ile	Cys	Ile	Ser	Leu	Tyr	Ala	Trp	Phe	Asp
				145					150					155	
Tyr	Ser	Met	Leu	His	Arg	Lys	His	Trp	Glu	His	His	Asn	His	Thr	Gly
				165					170					175	
Glu	Val	Gly	Lys	Asp	Pro	Asp	Phe	His	Lys	Gly	Asn	Pro	Gly	Leu	Val
				180					185					190	
Pro	Trp	Phe	Ala	Ser	Phe	Met	Ser	Ser	Tyr	Met	Ser	Leu	Trp	Gln	Phe
				195					200					205	
Ala	Arg	Leu	Ala	Trp	Trp	Ala	Val	Val	Met	Gln	Met	Leu	Gly	Ala	Pro
				210					215					220	
Met	Ala	Asn	Leu	Leu	Val	Phe	Met	Ala	Ala	Ala	Pro	Ile	Leu	Ser	Ala

225 230 235 240

Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro
245 250 255

Gly Pro Ala Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr
260 265 270

Ser Glu Ala Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp
275 280 285

Leu His Trp Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu
290 295 300

Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Leu Ala
305 310 315 320

<210> 15
<211> 729
<212> DNA
<213> Agrobacterium aurantiacum

<220>
<221> CDS
<222> (1)..(729)

<400> 15
atg agc gca cat gcc ctg ccc aag gca gat ctg acc gcc acc agc ctg 48
Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
1 5 10 15

atc gtc tcg ggc ggc atc atc gcc gct tgg ctg gcc ctg cat gtg cat 96
Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
20 25 30

gcg ctg tgg ttt ctg gac gca gcg gcg cat ccc atc ctg gcg atc gca	144
Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala	
35 40 45	
aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg	192
Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala	
50 55 60	
cat gac gcg atg cac ggg tcg gtg gtg ccg ggg cgt ccg cgc gcc aat	240
His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn	
65 70 75 80	
gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg	288
Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp	
85 90 95	
cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc	336
Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr	
100 105 110	
gac gac gac ccc gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc	384
Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala	
115 120 125	
cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc	432
Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro	
130 135 140	
gtc atc gtg acg gtc tat gcg ctg atc ctt ggg gat cgc tgg atg tac	480
Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr	
145 150 155 160	
gtg gtc ttc tgg ccg ctg ccg tcg atc ctg gcg tcg atc cag ctg ttc	528
Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe	
165 170 175	
gtg ttc ggc acc tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg	576
Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro	
180 185 190	

gac cgc cac aat gcg cgg tcg tcg cgg atc agc gac ccc gtg tcg ctg 624
Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
195 200 205

ctg acc tgc ttt cac ttt ggc ggt tat cat cac gaa cac cac ctg cac 672
Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
210 215 220

ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac 720
Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
225 230 235 240

acc gca tga 729
Thr Ala

<210> 16
<211> 242
<212> PRT
<213> Agrobacterium aurantiacum

<400> 16

Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
1 5 10 15

Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
20 25 30

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala
35 40 45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
65 70 75 80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
85 90 95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
130 135 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
180 185 190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
210 215 220

Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp

225

230

235

240

Thr Ala

<210> 17

<211> 1631

<212> DNA

<213> *Alcaligenes* sp.

<220>

<221> CDS

<222> (99)..(827)

<400> 17

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ccgggtctagg ctgtcgccct acgcagcagg agtttcgg atg tcc gga cgg aag cct 116

Met Ser Gly Arg Lys Pro

1

5

ggc aca act ggc gac acg atc gtc aat ctc ggt ctg acc gcc gcg atc 164

Gly Thr Thr Gly Asp Thr Ile Val Asn Leu Gly Leu Thr Ala Ala Ile

10

15

20

ctg ctg tgc tgg ctg gtc ctg cac gcc ttt acg cta tgg ttg cta gat 212

Leu Leu Cys Trp Leu Val Leu His Ala Phe Thr Leu Trp Leu Leu Asp

25

30

35

gcg gcc gcg cat ccg ctg ctt gcc gtg ctg tgc ctg gct ggg ctg acc 260

Ala Ala Ala His Pro Leu Leu Ala Val Leu Cys Leu Ala Gly Leu Thr

40

45

50

tgg ctg tcg gtc ggg ctg ttc atc atc gcg cat gac gca atg cac ggg 308

Trp Leu Ser Val Gly Leu Phe Ile Ile Ala His Asp Ala Met His Gly

55

60

65

70

tcc gtg gtg ccg ggg cgg ccg cgc gcc aat gcg gcg atc ggg caa ctg 356

Ser Val Val Pro Gly Arg Pro Arg Ala Asn Ala Ala Ile Gly Gln Leu	
75 80 85	
gcg ctg tgg ctc tat gcg ggg ttc tcg tgg ccc aag ctg atc gcc aag	404
Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp Pro Lys Leu Ile Ala Lys	
90 95 100	
cac atg acg cat cac cgg cac gcc ggc acc gac aac gat ccc gat ttc	452
His Met Thr His His Arg His Ala Gly Thr Asp Asn Asp Pro Asp Phe	
105 110 115	
ggt cac gga ggg ccc gtg cgc tgg tac ggc agc ttc gtc tcc acc tat	500
Gly His Gly Gly Pro Val Arg Trp Tyr Gly Ser Phe Val Ser Thr Tyr	
120 125 130	
ttc ggc tgg cga gag gga ctg ctg cta ccg gtg atc gtc acc acc tat	548
Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro Val Ile Val Thr Thr Tyr	
135 140 145 150	
gcg ctg atc ctg ggc gat cgc tgg atg tat gtc atc ttc tgg ccg gtc	596
Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr Val Ile Phe Trp Pro Val	
155 160 165	
ccg gcc gtt ctg gcg tcg atc cag att ttc gtc ttc gga act tgg ctg	644
Pro Ala Val Leu Ala Ser Ile Gln Ile Phe Val Phe Gly Thr Trp Leu	
170 175 180	
ccc cac cgc ccg gga cat gac gat ttt ccc gac cgg cac aac gcg agg	692
Pro His Arg Pro Gly His Asp Asp Phe Pro Asp Arg His Asn Ala Arg	
185 190 195	
tcg acc ggc atc ggc gac ccg ttg tca cta ctg acc tgc ttc cat ttc	740
Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu Leu Thr Cys Phe His Phe	
200 205 210	
ggc ggc tat cac cac gaa cat cac ctg cat ccg cat gtg ccg tgg tgg	788
Gly Gly Tyr His His Glu His His Leu His Pro His Val Pro Trp Trp	
215 220 225 230	
cgc ctg cct cgt aca cgc aag acc gga ggc cgc gca tga cgcaattcct	837
Arg Leu Pro Arg Thr Arg Lys Thr Gly Gly Arg Ala	

235

240

cattgtcgtg gcgacagtcc tcgtgatgga gctgaccgcc tattccgtcc accgctggat 897
tatgcacggc cccctaggct ggggctggca caagtcccat cacgaagagc acgaccacgc 957
gttgagagaag aacgacctct acggcgctcg cttcgcggtg ctggcgacga tcctcttcac 1017
cgtgggcgcc tattggtggc cgggtgctgtg gtggatcgcc ctgggcatga cggctctatgg 1077
gttgatctat ttcactctgc acgacgggct tgtgcatcaa cgctggccgt ttcgggtatat 1137
tccgcggcgg ggctatttcc gcaggctcta ccaagctcat cgctgcacc acgcggtcga 1197
ggggcgggac cactgcgtca gcttcggctt catctatgcc ccaccgtgg acaagctgaa 1257
gcaggatctg aagcggtcgg gtgtcctgcg cccccaggac gagcgtccgt cgtgatctct 1317
gatcccggcg tggccgcatg aaatccgacg tgctgctggc aggggcccgc cttgccaacg 1377
gactgatcgc gctggcgatc cgcaaggcgc ggcccgaact tcgctgctg ctgctggacc 1437
gtgcggcggg cgctcggac gggcatactt ggtcctgcca cgacaccgat ttggcgccgc 1497
actggctgga ccgcctgaag ccgatcaggc gtggcgactg gcccgatcag gaggtgcggt 1557
tcccagacca ttcgcgaagg ctccgggccg gatatggctc gatcgacggg cgggggctga 1617
tgctgctggt gacc 1631

<210> 18

<211> 242

<212> PRT

<213> *Alcaligenes* sp.

<400> 18

Met Ser Gly Arg Lys Pro Gly Thr Thr Gly Asp Thr Ile Val Asn Leu
1 5 10 15

Gly Leu Thr Ala Ala Ile Leu Leu Cys Trp Leu Val Leu His Ala Phe
20 25 30

Thr Leu Trp Leu Leu Asp Ala Ala Ala His Pro Leu Leu Ala Val Leu
35 40 45

Cys Leu Ala Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
65 70 75 80

Ala Ala Ile Gly Gln Leu Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp
85 90 95

Pro Lys Leu Ile Ala Lys His Met Thr His His Arg His Ala Gly Thr
100 105 110

Asp Asn Asp Pro Asp Phe Gly His Gly Gly Pro Val Arg Trp Tyr Gly
115 120 125

Ser Phe Val Ser Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
130 135 140

Val Ile Val Thr Thr Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145 150 155 160

Val Ile Phe Trp Pro Val Pro Ala Val Leu Ala Ser Ile Gln Ile Phe
165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Asp Phe Pro
180 185 190

Asp Arg His Asn Ala Arg Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu
195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
210 215 220

Pro His Val Pro Trp Trp Arg Leu Pro Arg Thr Arg Lys Thr Gly Gly
225 230 235 240

Arg Ala

<210> 19
<211> 729
<212> DNA
<213> *Paracoccus marcusii*

<220>
<221> CDS
<222> (1)..(729)

<400> 19
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Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
1 5 10 15

atc gtc tcg ggc ggc atc atc gcc gca tgg ctg gcc ctg cat gtg cat 96
Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
20 25 30

gcg ctg tgg ttt ctg gac gcg gcg gcc cat ccc atc ctg gcg gtc gcg 144

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Val Ala	
35 40 45	
aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg	192
Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala	
50 55 60	
cat gac gcg atg cac ggg tcg gtc gtg ccg ggg cgt ccg cgc gcc aat	240
His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn	
65 70 75 80	
gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg	288
Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp	
85 90 95	
cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc	336
Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr	
100 105 110	
gac gac gac cca gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc	384
Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala	
115 120 125	
cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc	432
Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro	
130 135 140	
gtc atc gtg acg gtc tat gcg ctg atc ctg ggg gat cgc tgg atg tac	480
Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr	
145 150 155 160	
gtg gtc ttc tgg ccg ttg ccg tcg atc ctg gcg tcg atc cag ctg ttc	528
Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe	
165 170 175	
gtg ttc ggc act tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg	576
Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro	
180 185 190	
gac cgc cat aat gcg cgg tcg tcg cgg atc agc gac cct gtg tcg ctg	624
Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu	

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
65 70 75 80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
85 90 95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
130 135 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
180 185 190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
210 215 220

Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
225 230 235 240

[illegible]

ctg gat ggc caa gct ttt atg agc tac cgt tcc cta gaa aaa acc tgt	336
Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys	
100 105 110	
gcc cac att gcc acc tat agc ccc cga gat gcg gaa aaa tat cgg caa	384
Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln	
115 120 125	
ttt gtc aat tat tgg acg gat ttg ctc aac gct gtc cag cct gct ttt	432
Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe	
130 135 140	
aat gct ccg ccc cag gct tta cta gat tta gcc ctg aac tat ggt tgg	480
Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp	
145 150 155 160	
gaa aac tta aaa tcc gtg ctg gcg atc gcc ggg tcg aaa acc aag gcg	528
Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala	
165 170 175	
ttg gat ttt atc cgc act atg atc ggc tcc ccg gaa gat gtg ctc aat	576
Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn	
180 185 190	
gaa tgg ttc gac agc gaa cgg gtt aaa gct cct tta gct aga cta tgt	624
Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys	
195 200 205	
tcg gaa att ggc gct ccc cca tcc caa aag ggt agt agc tcc ggc atg	672
Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met	
210 215 220	
atg atg gtg gcc atg cgg cat ttg gag gga att gcc aga cca aaa gga	720
Met Met Val Ala Met Arg His Leu Glu Gly Ile Ala Arg Pro Lys Gly	
225 230 235 240	
ggc act gga gcc ctc aca gaa gcc ttg gtg aag tta gtg caa gcc caa	768
Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln	
245 250 255	

ggg gga aaa atc ctc act gac caa acc gtc aaa cgg gta ttg gtg gaa	816
Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu	
260 265 270	
aac aac cag gcg atc ggg gtg gag gta gct aac gga gaa cag tac cgg	864
Asn Asn Gln Ala Ile Gly Val Glu Val Ala Asn Gly Glu Gln Tyr Arg	
275 280 285	
gcc aaa aaa ggc gtg att tct aac atc gat gcc cgc cgt tta ttt ttg	912
Ala Lys Lys Gly Val Ile Ser Asn Ile Asp Ala Arg Arg Leu Phe Leu	
290 295 300	
caa ttg gtg gaa ccg ggg gcc cta gcc aag gtg aat caa aac cta ggg	960
Gln Leu Val Glu Pro Gly Ala Leu Ala Lys Val Asn Gln Asn Leu Gly	
305 310 315 320	
gaa cga ctg gaa cgg cgc act gtg aac aat aac gaa gcc att tta aaa	1008
Glu Arg Leu Glu Arg Arg Thr Val Asn Asn Asn Glu Ala Ile Leu Lys	
325 330 335	
atc gat tgt gcc ctc tcc ggt tta ccc cac ttc act gcc atg gcc ggg	1056
Ile Asp Cys Ala Leu Ser Gly Leu Pro His Phe Thr Ala Met Ala Gly	
340 345 350	
ccg gag gat cta acg gga act att ttg att gcc gac tcg gta cgc cat	1104
Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His	
355 360 365	
gtc gag gaa gcc cac gcc ctc att gcc ttg ggg caa att ccc gat gct	1152
Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala	
370 375 380	
aat ccg tct tta tat ttg gat att ccc act gta ttg gac ccc acc atg	1200
Asn Pro Ser Leu Tyr Leu Asp Ile Pro Thr Val Leu Asp Pro Thr Met	
385 390 395 400	
gcc ccc cct ggg cag cac acc ctc tgg atc gaa ttt ttt gcc ccc tac	1248
Ala Pro Pro Gly Gln His Thr Leu Trp Ile Glu Phe Phe Ala Pro Tyr	
405 410 415	

cgc atc gcc ggg ttg gaa ggg aca ggg tta atg ggc aca ggt tgg acc 1296
Arg Ile Ala Gly Leu Glu Gly Thr Gly Leu Met Gly Thr Gly Trp Thr
420 425 430

gat gag tta aag gaa aaa gtg gcg gat cgg gtg att gat aaa tta acg 1344
Asp Glu Leu Lys Glu Lys Val Ala Asp Arg Val Ile Asp Lys Leu Thr
435 440 445

gac tat gcc cct aac cta aaa tct ctg atc att ggt cgc cga gtg gaa 1392
Asp Tyr Ala Pro Asn Leu Lys Ser Leu Ile Ile Gly Arg Arg Val Glu
450 455 460

agt ccc gcc gaa ctg gcc caa cgg ctg gga agt tac aac ggc aat gtc 1440
Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val
465 470 475 480

tat cat ctg gat atg agt ttg gac caa atg atg ttc ctc cgg cct cta 1488
Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu
485 490 495

ccg gaa att gcc aac tac caa acc ccc atc aaa aat ctt tac tta aca 1536
Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr
500 505 510

ggg gcg ggt acc cat ccc ggt ggc tcc ata tca ggt atg ccc ggt aga 1584
Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg
515 520 525

aat tgc gct cgg gtc ttt tta aaa caa caa cgt cgt ttt tgg taa 1629
Asn Cys Ala Arg Val Phe Leu Lys Gln Gln Arg Arg Phe Trp
530 535 540

<210> 22

<211> 542

<212> PRT

<213> Synechocystis sp.

<400> 22

Met Ile Thr Thr Asp Val Val Ile Ile Gly Ala Gly His Asn Gly Leu
1 5 10 15

Val Cys Ala Ala Tyr Leu Leu Gln Arg Gly Leu Gly Val Thr Leu Leu
20 25 30

Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met
35 40 45

Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His
50 55 60

Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln
65 70 75 80

Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly
85 90 95

Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys
100 105 110

Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln
115 120 125

Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe
130 135 140

Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp
145 150 155 160

Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala
165 170 175

Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn
180 185 190

Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys
195 200 205

Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met
210 215 220

Met Met Val Ala Met Arg His Leu Glu Gly Ile Ala Arg Pro Lys Gly
225 230 235 240

Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln
245 250 255

Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu
260 265 270

Asn Asn Gln Ala Ile Gly Val Glu Val Ala Asn Gly Glu Gln Tyr Arg
275 280 285

Ala Lys Lys Gly Val Ile Ser Asn Ile Asp Ala Arg Arg Leu Phe Leu
290 295 300

Gln Leu Val Glu Pro Gly Ala Leu Ala Lys Val Asn Gln Asn Leu Gly
305 310 315 320

Glu Arg Leu Glu Arg Arg Thr Val Asn Asn Asn Glu Ala Ile Leu Lys

325

330

335

Ile Asp Cys Ala Leu Ser Gly Leu Pro His Phe Thr Ala Met Ala Gly
340 345 350

Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His
355 360 365

Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala
370 375 380

Asn Pro Ser Leu Tyr Leu Asp Ile Pro Thr Val Leu Asp Pro Thr Met
385 390 395 400

Ala Pro Pro Gly Gln His Thr Leu Trp Ile Glu Phe Phe Ala Pro Tyr
405 410 415

Arg Ile Ala Gly Leu Glu Gly Thr Gly Leu Met Gly Thr Gly Trp Thr
420 425 430

Asp Glu Leu Lys Glu Lys Val Ala Asp Arg Val Ile Asp Lys Leu Thr
435 440 445

Asp Tyr Ala Pro Asn Leu Lys Ser Leu Ile Ile Gly Arg Arg Val Glu
450 455 460

Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val
465 470 475 480

Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu
485 490 495

Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr
500 505 510

Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg
515 520 525

Asn Cys Ala Arg Val Phe Leu Lys Gln Gln Arg Arg Phe Trp
530 535 540

<210> 23
<211> 776
<212> DNA
<213> Bradyrhizobium sp.

<220>
<221> CDS
<222> (1)..(774)

<400> 23
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Met His Ala Ala Thr Ala Lys Ala Thr Glu Phe Gly Ala Ser Arg Arg
1 5 10 15
gac gat gcg agg cag cgc cgc gtc ggt ctc acg ctg gcc gcg gtc atc 96
Asp Asp Ala Arg Gln Arg Arg Val Gly Leu Thr Leu Ala Ala Val Ile
20 25 30
atc gcc gcc tgg ctg gtg ctg cat gtc ggt ctg atg ttc ttc tgg ccg 144
Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro
35 40 45
ctg acc ctt cac agc ctg ctg ccg gct ttg cct ctg gtg gtg ctg cag 192
Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln
50 55 60

acc tgg ctc tat gta ggc ctg ttc atc atc gcg cat gac tgc atg cac	240
Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His	
65 70 75 80	
ggc tcg ctg gtg ccg ttc aag ccg cag gtc aac cgc cgt atc gga cag	288
Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln	
85 90 95	
ctc tgc ctg ttc ctc tat gcc ggg ttc tcc ttc gac gct ctc aat gtc	336
Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val	
100 105 110	
gag cac cac aag cat cac cgc cat ccc ggc acg gcc gag gat ccc gat	384
Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp	
115 120 125	
ttc gac gag gtg ccg ccg cac ggc ttc tgg cac tgg ttc gcc agc ttt	432
Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe	
130 135 140	
ttc ctg cac tat ttc ggc tgg aag cag gtc gcg atc atc gca gcc gtc	480
Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val	
145 150 155 160	
tcg ctg gtt tat cag ctc gtc ttc gcc gtt ccc ttg cag aac atc ctg	528
Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu	
165 170 175	
ctg ttc tgg gcg ctg ccc ggg ctg ctg tcg gcg ctg cag ctg ttc acc	576
Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr	
180 185 190	
ttc ggc acc tat ctg ccg cac aag ccg gcc acg cag ccc ttc gcc gat	624
Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp	
195 200 205	
cgc cac aac gcg cgg acg agc gaa ttt ccc gcg tgg ctg tcg ctg ctg	672
Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu	
210 215 220	
acc tgc ttc cac ttc ggc ttt cat cac gag cat cat ctg cat ccc gat	720

Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp
225 230 235 240

gcg ccg tgg tgg cgg ctg ccg gag atc aag cgg cgg gcc ctg gaa agg 768
Ala Pro Trp Trp Arg Leu Pro Glu Ile Lys Arg Arg Ala Leu Glu Arg
245 250 255

cgt gac ta 776
Arg Asp

<210> 24
<211> 258
<212> PRT
<213> Bradyrhizobium sp.

<400> 24

Met His Ala Ala Thr Ala Lys Ala Thr Glu Phe Gly Ala Ser Arg Arg
1 5 10 15

Asp Asp Ala Arg Gln Arg Arg Val Gly Leu Thr Leu Ala Ala Val Ile
20 25 30

Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro
35 40 45

Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln
50 55 60

Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His
65 70 75 80

Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln
85 90 95

Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val
100 105 110

Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp
115 120 125

Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe
130 135 140

Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val
145 150 155 160

Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu
165 170 175

Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr
180 185 190

Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp
195 200 205

Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu
210 215 220

Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp
225 230 235 240

Ala Pro Trp Trp Arg Leu Pro Glu Ile Lys Arg Arg Ala Leu Glu Arg
245 250 255

[illegible]

Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys	
100 105 110	
gat tta ttg aaa aaa cat tgg tta cac cac gga cat cct ggt act gat	384
Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp	
115 120 125	
tta gac cct gat tat tac aat ggt cat ccc caa aac ttc ttt ctt tgg	432
Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp	
130 135 140	
tat cta cat ttt atg aag tct tat tgg cga tgg acg caa att ttc gga	480
Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly	
145 150 155 160	
tta gtg atg att ttt cat gga ctt aaa aat ctg gtg cat ata cca gaa	528
Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu	
165 170 175	
aat aat tta att ata ttt tgg atg ata cct tct att tta agt tca gta	576
Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val	
180 185 190	
caa cta ttt tat ttt ggt aca ttt ttg cct cat aaa aag cta gaa ggt	624
Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly	
195 200 205	
ggt tat act aac ccc cat tgt gcg cgc agt atc cca tta cct ctt ttt	672
Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe	
210 215 220	
tgg tct ttt gtt act tgt tat cac ttc ggc tac cac aag gaa cat cac	720
Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His	
225 230 235 240	
gaa tac cct caa ctt cct tgg tgg aaa tta cct gaa gct cac aaa ata	768
Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile	
245 250 255	
tct tta taa	777
Ser Leu	

<210> 26

<211> 258

<212> PRT

<213> Nostoc sp.

<400> 26

Met Val Gln Cys Gln Pro Ser Ser Leu His Ser Glu Lys Leu Val Leu
1 5 10 15

Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe
20 25 30

Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu
35 40 45

Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala
50 55 60

Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
65 70 75 80

Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn
85 90 95

Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys
100 105 110

Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp
115 120 125

Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp

130

135

140

Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly

145

150

155

160

Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu

165

170

175

Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val

180

185

190

Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly

195

200

205

Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe

210

215

220

Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His

225

230

235

240

Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile

245

250

255

Ser Leu

<210> 27

<211> 789

<212> DNA

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Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe
130 135 140

atg ata gaa tac tcc agt tgg caa cag tta ata gta cta act atc cta 480
Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu
145 150 155 160

ttt aat tta gct aaa tac gtt ttg cac atc cat caa ata aat ctc atc 528
Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile
165 170 175

tta ttt tgg agt att cct cca att tta agt tcc att caa ctg ttt tat 576
Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr
180 185 190

ttc gga aca ttt ttg cct cat cga gaa ccc aag aaa gga tat gtt tat 624
Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr
195 200 205

ccc cat tgc agc caa aca ata aaa ttg cca act ttt ttg tca ttt atc 672
Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile
210 215 220

gct tgc tac cac ttt ggt tat cat gaa gaa cat cat gag tat ccc cat 720
Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
225 230 235 240

gta cct tgg tgg caa ctt cca tct gta tat aag cag aga gta ttc aac 768
Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn
245 250 255

aat tca gta acc aat tcg taa 789
Asn Ser Val Thr Asn Ser
260

<210> 28
<211> 262
<212> PRT
<213> Nostoc punctiforme

<400> 28

Leu Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln
1 5 10 15

Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val
20 25 30

Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn
35 40 45

Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln
50 55 60

Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His
65 70 75 80

Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser
85 90 95

Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys
100 105 110

Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp
115 120 125

Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe
130 135 140

Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu
145 150 155 160

Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile
165 170 175

Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr
180 185 190

Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr
195 200 205

Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile
210 215 220

Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
225 230 235 240

Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn
245 250 255

Asn Ser Val Thr Asn Ser
260

<210> 29
<211> 762
<212> DNA
<213> Nostoc punctiforme

<220>
<221> CDS
<222> (1)..(762)

<400> 29
gtg atc cag tta gaa caa cca ctc agt cat caa gca aaa ctg act cca

Val	Ile	Gln	Leu	Glu	Gln	Pro	Leu	Ser	His	Gln	Ala	Lys	Leu	Thr	Pro		
1				5					10					15			
gta ctg aga agt aaa tct cag ttt aag ggg ctt ttc att gct att gtc																	96
Val	Leu	Arg	Ser	Lys	Ser	Gln	Phe	Lys	Gly	Leu	Phe	Ile	Ala	Ile	Val		
			20					25					30				
att gtt agc gca tgg gtc att agc ctg agt tta tta ctt tcc ctt gac																	144
Ile	Val	Ser	Ala	Trp	Val	Ile	Ser	Leu	Ser	Leu	Leu	Leu	Ser	Leu	Asp		
			35					40					45				
atc tca aag cta aaa ttt tgg atg tta ttg cct gtt ata cta tgg caa																	192
Ile	Ser	Lys	Leu	Lys	Phe	Trp	Met	Leu	Leu	Pro	Val	Ile	Leu	Trp	Gln		
		50				55					60						
aca ttt tta tat acg gga tta ttt att aca tct cat gat gcc atg cat																	240
Thr	Phe	Leu	Tyr	Thr	Gly	Leu	Phe	Ile	Thr	Ser	His	Asp	Ala	Met	His		
65					70				75					80			
ggc gta gta ttt ccc caa aac acc aag att aat cat ttg att gga aca																	288
Gly	Val	Val	Phe	Pro	Gln	Asn	Thr	Lys	Ile	Asn	His	Leu	Ile	Gly	Thr		
			85					90					95				
ttg acc cta tcc ctt tat ggt ctt tta cca tat caa aaa cta ttg aaa																	336
Leu	Thr	Leu	Ser	Leu	Tyr	Gly	Leu	Leu	Pro	Tyr	Gln	Lys	Leu	Leu	Lys		
			100					105					110				
aaa cat tgg tta cac cac cac aat cca gca agc tca ata gac ccg gat																	384
Lys	His	Trp	Leu	His	His	His	Asn	Pro	Ala	Ser	Ser	Ile	Asp	Pro	Asp		
		115					120					125					
ttt cac aat ggt aaa cac caa agt ttc ttt gct tgg tat ttt cat ttt																	432
Phe	His	Asn	Gly	Lys	His	Gln	Ser	Phe	Phe	Ala	Trp	Tyr	Phe	His	Phe		
		130				135					140						
atg aaa ggt tac tgg agt tgg ggg caa ata att gcg ttg act att att																	480
Met	Lys	Gly	Tyr	Trp	Ser	Trp	Gly	Gln	Ile	Ile	Ala	Leu	Thr	Ile	Ile		
145					150				155				160				
tat aac ttt gct aaa tac ata ctc cat atc cca agt gat aat cta act																	528
Tyr	Asn	Phe	Ala	Lys	Tyr	Ile	Leu	His	Ile	Pro	Ser	Asp	Asn	Leu	Thr		

Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Leu Ser Leu Asp

35

40

45

Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln
50 55 60

Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His
65 70 75 80

Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr
85 90 95

Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys
100 105 110

Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp
115 120 125

Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe
130 135 140

Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile
145 150 155 160

Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr
165 170 175

Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr
180 185 190

Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln
195 200 205

Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile
210 215 220

Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
225 230 235 240

Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys
245 250

<210> 31
<211> 1608
<212> DNA
<213> Haematococcus pluvialis

<220>
<221> CDS
<222> (3)..(971)

<400> 31
ct aca ttt cac aag ccc gtg agc ggt gca agc gct ctg ccc cac atc 47
Thr Phe His Lys Pro Val Ser Gly Ala Ser Ala Leu Pro His Ile
1 5 10 15
ggc cca cct cct cat ctc cat cgg tca ttt gct gct acc acg atg ctg 95
Gly Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu
20 25 30
tcg aag ctg cag tca atc agc gtc aag gcc cgc cgc gtt gaa cta gcc 143
Ser Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala
35 40 45
cgc gac atc acg cgg ccc aaa gtc tgc ctg cat gct cag cgg tgc tcg 191
Arg Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser
50 55 60

tta gtt cgg ctg cga gtg gca gca cca cag aca gag gag gcg ctg gga	239
Leu Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly	
65 70 75	
acc gtg cag gct gcc ggc gcg ggc gat gag cac agc gcc gat gta gca	287
Thr Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala	
80 85 90 95	
ctc cag cag ctt gac cgg gct atc gca gag cgt cgt gcc cgg cgc aaa	335
Leu Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys	
100 105 110	
cgg gag cag ctg tca tac cag gct gcc gcc att gca gca tca att ggc	383
Arg Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly	
115 120 125	
gtg tca ggc att gcc atc ttc gcc acc tac ctg aga ttt gcc atg cac	431
Val Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His	
130 135 140	
atg acc gtg ggc ggc gca gtg cca tgg ggt gaa gtg gct ggc act ctc	479
Met Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu	
145 150 155	
ctc ttg gtg gtt ggt ggc gcg ctc ggc atg gag atg tat gcc cgc tat	527
Leu Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr	
160 165 170 175	
gca cac aaa gcc atc tgg cat gag tcg cct ctg ggc tgg ctg ctg cac	575
Ala His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His	
180 185 190	
aag agc cac cac aca cct cgc act gga ccc ttt gaa gcc aac gac ttg	623
Lys Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu	
195 200 205	
ttt gca atc atc aat gga ctg ccc gcc atg ctc ctg tgt acc ttt ggc	671
Phe Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly	
210 215 220	
ttc tgg ctg ccc aac gtc ctg ggg gcg gcc tgc ttt gga gcg ggg ctg	719

Phe Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu	
225	230 235
ggc atc acg cta tac ggc atg gca tat atg ttt gta cac gat ggc ctg	767
Gly Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu	
240	245 250 255
gtg cac agg cgc ttt ccc acc ggg ccc atc gct ggc ctg ccc tac atg	815
Val His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met	
	260 265 270
aag cgc ctg aca gtg gcc cac cag cta cac cac agc ggc aag tac ggt	863
Lys Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly	
	275 280 285
ggc gcg ccc tgg ggt atg ttc ttg ggt cca cag gag ctg cag cac att	911
Gly Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile	
	290 295 300
cca ggt gcg gcg gag gag gtg gag cga ctg gtc ctg gaa ctg gac tgg	959
Pro Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp	
	305 310 315
tcc aag cgg tag ggtgcggaac caggcacgct gggtttcacac ctcatgcctg	1011
Ser Lys Arg	
320	
tgataagggtg tggctagagc gatgcgtgtg agacgggtat gtcacggtcg actggtctga	1071
tggccaatgg catcggccat gtctggtcat cacgggctgg ttgcctgggt gaagggtgatg	1131
cacatcatca tgtgcggttg gaggggctgg cacagtgtgg gctgaactgg agcagttgtc	1191
caggctggcg ttgaatcagt gagggtttgt gattggcggg tgtgaagcaa tgactccgcc	1251
catattctat ttgtgggagc tgagatgatg gcatgcttgg gatgtgcatg gatcatggta	1311
gtgcagcaaaa ctatattcac ctagggtgtg tggtaggatc aggtgaggcc ttgcacattg	1371
catgatgtac tcgtcatggt gtgttggtga gaggatggat gtggatggat gtgtattctc	1431

agacgtagac cttgactgga ggcttgatcg agagagtggg ccgtattctt tgagagggga 1491

ggctcgtgcc agaaatggtg agtggatgac tgtgacgctg tacattgcag gcaggtgaga 1551

tgcactgtct cgattgtaaa atacattcag atgcaaaaaa aaaaaaaaaa aaaaaaa 1608

<210> 32

<211> 322

<212> PRT

<213> Haematococcus pluvialis

<400> 32

Thr Phe His Lys Pro Val Ser Gly Ala Ser Ala Leu Pro His Ile Gly
1 5 10 15

Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu Ser
20 25 30

Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala Arg
35 40 45

Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser Leu
50 55 60

Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly Thr
65 70 75 80

Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala Leu
85 90 95

Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys Arg
100 105 110

Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly Val
115 120 125

Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His Met
130 135 140

Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu Leu
145 150 155 160

Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr Ala
165 170 175

His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His Lys
180 185 190

Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu Phe
195 200 205

Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly Phe
210 215 220

Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu Gly
225 230 235 240

Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu Val
245 250 255

His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met Lys
260 265 270

Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly Gly
275 280 285

Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile Pro
290 295 300

Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp Ser
305 310 315 320

Lys Arg

<210> 33

<211> 528

<212> DNA

<213> Erwinia uredovora

<220>

<221> CDS

<222> (1)..(528)

<400> 33

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Met Leu Trp Ile Trp Asn Ala Leu Ile Val Phe Val Thr Val Ile Gly
1 5 10 15

atg gaa gtg att gct gca ctg gca cac aaa tac atc atg cac ggc tgg 96
Met Glu Val Ile Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp
20 25 30

ggc tgg gga tgg cat ctt tca cat cat gaa ccg cgt aaa ggt gcg ttt 144
Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
35 40 45

gaa gtt aac gat ctt tat gcc gtg gtt ttt gct gca tta tcg atc ctg 192
Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ala Leu Ser Ile Leu

50	55	60	
ctg att tat ctg ggc agt aca gga atg tgg ccg ctc cag tgg att ggc	240		
Leu Ile Tyr Leu Gly Ser Thr Gly Met Trp Pro Leu Gln Trp Ile Gly			
65 70 75 80			
gca ggt atg acg gcg tat gga tta ctc tat ttt atg gtg cac gac ggg	288		
Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly			
85 90 95			
ctg gtg cat caa cgt tgg cca ttc cgc tat att cca cgc aag ggc tac	336		
Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr			
100 105 110			
ctc aaa cgg ttg tat atg gcg cac cgt atg cat cac gcc gtc agg ggc	384		
Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly			
115 120 125			
aaa gaa ggt tgt gtt tct ttt ggc ttc ctc tat gcg ccg ccc ctg tca	432		
Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser			
130 135 140			
aaa ctt cag gcg acg ctc cgg gaa aga cat ggc gct aga gcg ggc gct	480		
Lys Leu Gln Ala Thr Leu Arg Glu Arg His Gly Ala Arg Ala Gly Ala			
145 150 155 160			
gcc aga gat gcg cag ggc ggg gag gat gag ccc gca tcc ggg aag taa	528		
Ala Arg Asp Ala Gln Gly Gly Glu Asp Glu Pro Ala Ser Gly Lys			
165 170 175			

<210> 34
 <211> 175
 <212> PRT
 <213> Erwinia uredovora

<400> 34

Met Leu Trp Ile Trp Asn Ala Leu Ile Val Phe Val Thr Val Ile Gly
1 5 10 15

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<211> 500

<212> DNA

<213> Blakeslea trispora

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<213> Blakeslea trispora

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<210> 67

<211> 720

<212> DNA

<213> *Blakeslea trispora*

<400> 67

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<212> DNA
<213> Blakeslea trispora

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<210> 69
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<213> Blakeslea trispora

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<211> 882

<212> DNA

<213> Haematococcus pluvialis

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<210> 71

<211> 528

<212> DNA

<213> *Erwinia uredovora*

<400> 71

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<211> 762

<212> DNA

<213> *Nostoc sp. PCC73102*

<400> 72

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<211> 617

<212> DNA

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<400> 73

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<213> Blakeslea trispora

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